

## SEQUENCE LISTING

<110> De Buyl, Eric  
Lahaye, Andree  
Ledoux, Pierre  
Detroz, Rene

<120> Xylanase, Microorganisms Producing it,  
DNA Molecules, Methods for Preparing this Xylanase and Uses  
of the Latter

<130> GC450-D1-US

<140> US 09/909,207  
<141> 2001-07-19

<150> US 08/470,953  
<151> 1995-06-06

<150> BE 09500448  
<151> 1995-05-17

<150> BE 09400706  
<151> 1994-07-26

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aacaatgtta acaacatatt atccgtaaa ggtaaaaat tcaatgaaac acaaacacac 180  
caacaagtgg ttaacatgtc cataaactac ggagccaact tccaaacccaa tggtaatgcg 240  
tatttatgcg tctatggttg gactgttgac cctcttgcg aatattatat tgtcgacagt 300  
tggggcaact ggcgtccacc aggagaacg cctaaggggg ccatacactgt tgatggagga 360  
acatatgata tctacgagac tcttagatgc aatcaaccct ccattaaggg gattgccaca 420  
tttaaacaat attggagtgt tcgaagatcg aaacgcacga gtggcacat ttctgtcagc 480  
aaccacttta gagcgtggga aaacttaggg atgaatatgg ggaaaaatgtt tgaagtgcgc 540  
cttactgttag aaggctatca aagtagcgga agtgcataatg tatataccaa tacactaaga 600  
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<222> (1)...(663)

<221> mat\_peptide  
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gaa ttt tgg aaa gat agc ggt ggc tct ggg aca atg att ctc aat cat		96
Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His		
20 25 30		
gga ggt acg ttc agt gcc caa tgg aac aat gtt aac aac ata tta ttc		144
Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe		
35 40 45		
cgt aaa ggt aaa aaa ttc aat gaa aca caa aca cac caa caa gtt ggt		192
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly		
50 55 60		
aac atg tcc ata aac tac gga gcc aac ttc caa cca aat ggt aat gcg		240
Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala		
65 70 75 80		
tat tta tgc gtc tat ggt tgg act gtt gac cct ctt gtc gaa tat tat		288
Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr		
85 90 95		
att gtc gac agt tgg ggc aac tgg cgt cca cca gga gca acg cct aag		336
Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys		
100 105 110		
ggg acc atc act gtt gat gga gga aca tat gat atc tac gag act ctt		384
Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu		
115 120 125		
aga gtc aat caa ccc tcc att aag ggg att gcc aca ttt aaa caa tat		432
Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr		
130 135 140		
tgg agt gtt cga aga tcg aaa cgc acg agt ggc acg att tct gtc agc		480
Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser		
145 150 155 160		
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Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met		
165 170 175		
tat gaa gtc gcg ctt act gta gaa ggc tat caa agt agc gga agt gct		576
Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala		
180 185 190		
aat gta tat agc aat aca cta aga att aac ggt aac cct ctc tca act		624
Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr		
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663

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 Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe  
 35 40 45  
 Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly  
 50 55 60  
 Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala  
 65 70 75 80  
 Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr  
 85 90 95  
 Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys  
 100 105 110  
 Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu  
 115 120 125  
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 130 135 140  
 Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser  
 145 150 155 160  
 Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met  
 165 170 175  
 Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala  
 180 185 190  
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 210 215 220

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 ggtacgttca gtgcccaatg gaacaatgtt aacaacatat tattccgtaa agttaaaaaa 240  
 ttcaatgaaa cacaaacaca ccaacaatgtt gtaacatgtt ccataaacta cggagccaac 300  
 ttccaaaccctt atggtaatgc gtatttatgc gtctatgggtt ggacttgaa ccctcttgc 360  
 gaatattata ttgtcgacag ttggggcaac tgccgtccac caggagcaac gcctaagggg 420  
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 gggaaaatgtt atgaagtcgc gcttactgtt gaaggctatac aaagtagcgg aagtgtataat 660

gtatatacgca atacactaag aattaacggt aaccctctct caactattag taatgacgag 720  
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 1 5 10 15

gca cta acc tta cct gca gaa ata att cag gca caa atc gtc acc gac 96  
 Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala Gln Ile Val Thr Asp  
 20 25 30

aat tcc att ggc aac cac gat ggc tat gat tat gaa ttt tgg aaa gat 144  
 Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp  
 35 40 45

agc ggt ggc tct ggg aca atg att ctc aat cat ggc ggt acg ttc agt 192  
 Ser Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser  
 50 55 60

gcc caa tgg aac aat gtt aac aac ata tta ttc cgt aaa ggt aaa aaa 240  
 Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys  
 65 70 75 80

ttc aat gaa aca caa aca cac caa gtt ggt aac atg tcc ata aac 288  
 Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn  
 85 90 95

tac gga gcc aac ttc caa cca aat ggt aat gcg tat tta tgc gtc tat 336  
 Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr  
 100 105 110

ggg tgg act gtt gac cct ctt gtc gaa tat tat att gtc gac agt tgg 384  
 Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp  
 115 120 125

ggc aac tgg cgt cca cca gga gca acg cct aag ggg acc atc act gtt 432  
 Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val  
 130 135 140

gat gga gga aca tat gat atc tac gag act ctt aga gtc aat caa ccc 480  
 Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro

145	150	155	160	
tcc att aag ggg att gcc aca ttt aaa caa tat tgg agt gtt cga aga Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg 165 170 175				528
tcg aaa cgc acg agt ggc acg att tct gtc agc aac cac ttt aga gcg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala 180 185 190				576
tgg gaa aac tta ggg atg aat atg ggg aaa atg tat gaa gtc gcg ctt Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu 195 200 205				624
act gta gaa ggc tat caa agt agc gga agt gct aat gta tat agc aat Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn 210 215 220				672
aca cta aga att aac ggt aac cct ctc tca act att agt aat gac gag Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu 225 230 235 240				720
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20 25 30			
Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp			
35 40 45			
Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser			
50 55 60			
Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys			
65 70 75 80			
Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn			
85 90 95			
Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr			
100 105 110			
Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp			
115 120 125			
Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val			
130 135 140			
Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro			
145 150 155 160			
Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg			
165 170 175			
Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala			
180 185 190			

Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu  
 195 200 205  
 Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn  
 210 215 220  
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 Ser Ile Thr Leu Asp Lys Asn Asn  
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<213> Bacillus sp.

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<213> Bacillus sp.

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<210> 9  
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<212> PRT  
<213> Bacillus sp.

<400> 9  
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ccttgatcg	ttt aactttattt ttatcacaag aacattctt	240
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atttatgtca tattttctca cgccgc	tttcaaaaata cctgaagaac	360
ttaagtaat tagtatatac ttgcgttatac	aaaatgtgag ataatcta	420
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ctgtgaaagg aggtaggta gtaccgtaga cttcattacc	aaaaattagt tgtaaaaaaa	600
ttaaaaggag gaatgcctaa tgagacaaa gaaattgacg	ttgatttttag ccttttagt	660
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cattggcaac cacgtggct atgattatga atttggaaa	gatagcggtg gctctggac	780
aatgatttca aatcatggcg gtacgttca	tgcccaatgg aacaatgtt acaacatatt	840
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aaacttaggg atgaatatgg ggaaaatgtt tgaagtcgc	cttactgttag aaggtatca	1260
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<213> Bacillus sp.

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<221> sig\_peptide  
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ataggaactt tcccatttgc aagacgataa aaaatctttt	tccctat	240
ccttgatcg	ttt aactttattt ttatcacaag aacattctt	300
cattaatcac agttaacgct agagtcatct ttttcgg	ttt ctcatac	360
atttatgtca tattttctca cgccgc	tttcaaaaata cctgaagaac	420
ttaagtaat tagtatatac ttgcgttatac	aaaatgtgag ataatcta	480
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gataattatc cagtttcaaa atttgaata	gtgtgtatgg aatagttga atgtcaactg	600
ctgtgaaagg aggtaggta gtaccgtaga cttcattacc	aaaaattagt tgtaaaaaaa	662
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Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala

1

5

10

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caa atc gtc acc gac aat tcc att ggc aac cac gat ggc tat gat tat Gln Ile Val Thr Asp Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr 30 35 40	748
gaa ttt tgg aaa gat agc ggt ggc tct ggg aca atg att ctc aat cat Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His 45 50 55	796
ggc ggt acg ttc agt gcc caa tgg aac aat gtt aac aac ata tta ttc Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Asn Asn Ile Leu Phe 60 65 70 75	844
cgt aaa ggt aaa aaa ttc aat gaa aca caa aca cac caa caa gtt ggt Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly 80 85 90	892
aac atg tcc ata aac tac gga gcc aac ttc caa cca aat ggt aat gcg Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala 95 100 105	940
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att gtc gac agt tgg ggc aac tgg cgt cca cca gga gca acg cct aag Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys 125 130 135	1036
ggg acc atc act gtt gat gga gga aca tat gat atc tac gag act ctt Gly Thr Ile Thr Val Asp Gly Thr Tyr Asp Ile Tyr Glu Thr Leu 140 145 150 155	1084
aga gtc aat caa ccc tcc att aag ggg att gcc aca ttt aaa caa tat Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr 160 165 170	1132
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Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn  
240 245

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<213> Bacillus sp.

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ataggaactt tcccatttgc aagacgataa aaaatctttt tccccatTTT tatcttatcg 180  
ccttgatcggtt ttaatttgt aaactttattt tttagttacg tgatgtttcc tcattcatac 240  
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gataattatc cagtttcaaa atttggaaata gtgtgtatgg aatagtttga atgtcaactg 540  
ctgtgaaagg aggtaggta gtaccgtaga cttcattacc aaaaatttagt tgtaaaaaaaaaa 600  
ttaaaaggag gaatgccta 619

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<211> 150  
<212> DNA  
<213> Bacillus sp.

<400> 13  
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gaggaatgt tgaaaacacct ccgtcactag 150

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic oligonucleotide

<400> 14  
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<210> 15  
<211> 56  
<212> DNA  
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<220>  
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<400> 15  
ccccctacg taggccccgggg cggccggcgggt taccttagggc ctcgtgatac gcctat 56

<210> 16  
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<212> DNA  
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<220>  
<223> synthetic oligonucleotide

<400> 16  
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<210> 17  
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<213> Artificial Sequence

<220>  
<223> synthetic oligonucleotide

<400> 17  
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19

<210> 18  
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<220>  
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18

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36

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<220>  
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39

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<212> DNA  
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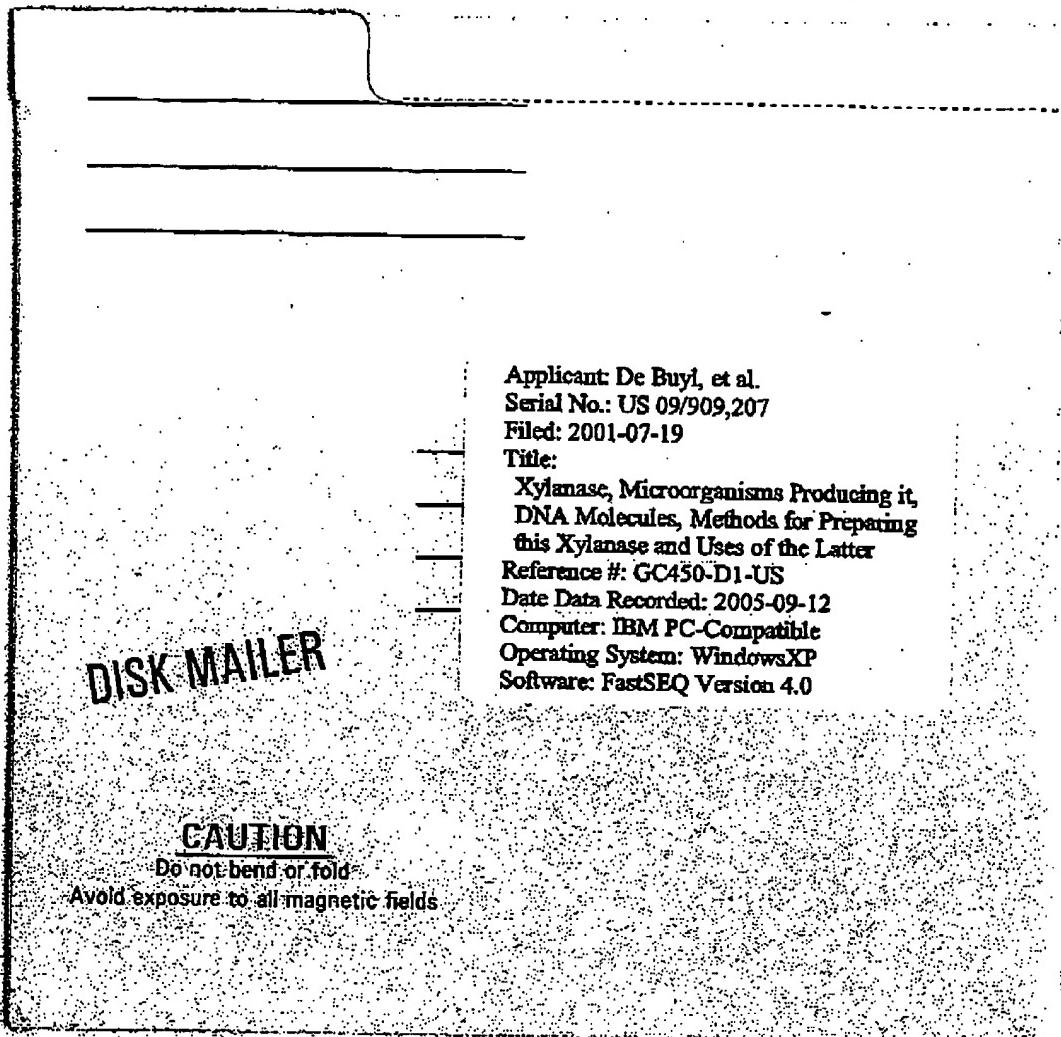
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